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Distoseptispora longispora sp. nov. from freshwater habitats in China

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Abstract—A novel species, *Distoseptispora longispora*, from submerged wood in Yunnan Province, China, is described and illustrated. The fungus is characterized by macronematous, mononematous, septate conidiophores with monoblastic, integrated, determinate, terminal conidiogenous cells that produce acrogenous, solitary, obclavate, elongated, distoseptate conidia. SSU-ITS-LSU sequence analyses were used to infer the phylogenetic relationship between *D. longispora* and related species. Both molecular analyses and morphological data well support *D. longispora* as an independent taxon. A key to *Distoseptispora* species is provided.

Key words—*Ascomycota,* asexual fungi, *Distoseptisporaceae,* hyphomycetes

Introduction

Distoseptispora K.D. Hyde & al. was introduced by Su & al. (2016) to accommodate two species, *D. fluminicola* McKenzie & al., the type species,

and *D. aquatica* Z.L. Luo & al. The genus is characterized by hairy colonies, macronematous conidiophores, monoblastic conidiogenous cells, and distoseptate acrogenous cylindrical conidia., *Distoseptispora* represents a phylogenetically distinct lineage in *Sordariomycetes* for which Su & al. (2016) proposed a new family, *Distoseptisporaceae* K.D. Hyde & McKenzie. Subsequently, 13 more species have been added: *D. cangshanensis* Z.L. Luo & al., *D. dehongensis* W. Dong & al., *D. guttulata* Jing Yang & K.D. Hyde, *D. martinii* (J.L. Crane & Dumont) J.W. Xia & X.G. Zhang, *D. obpyriformis* Z.L. Luo & H.Y. Su, *D. palmarum* S.N. Zhang & al., *D. phangngaensis* Jing Yang & al., *D. rostrata* Z.L. Luo & al., *D. submersa* Z.L. Luo & al., *D. suoluoensis* Jing Yang & al., *D. thailandica* Tibpromma & K.D. Hyde, *D. thysanolaenae* Goonas. & al., and *D. xishuangbannaensis* Tibpromma & K.D. Hyde (Hyde & al. 2019, Luo & al. 2018, Phookamsak & al. 2019, Tibpromma & al 2018, Xia & al. 2017, Yang & al. 2018).

Many aquatic fungi have been discovered in China's freshwater habitats, which are rich in lignicolous fungi (Hu & al. 2007, 2012a,b; Huang & al. 2016; Song & al. 2018). Our ongoing survey of aquatic fungi in Yunnan Province revealed an interesting *Distoseptispora* species that we describe as new based on morphological characters and molecular analyses (SSU-ITS-LSU).

Materials & methods

Sample collection & morphological studies

Debarked wood samples from different freshwater habitats in Yunnan Province, China, were taken to the lab for detection of fungi using dissecting and compound microscopes. The dried specimens were deposited in the Herbarium of Fungi, Jiangxi Agricultural University, Nanchang, China (HFJAU).

DNA extraction, sequencing, and phylogenetic analyses

Genomic DNA was extracted from fresh fungal materials found on the natural substrate following Hu & al. (2012c). We amplified three rDNA regions: internal

Table 1. Isolates included in the phylogenetic analyses.

Species	Strain	GenBank accession numbers		
		ITS	LSU	SSU
Distoseptispora "*adscendens*"	HKUCC 10820	—	DQ408561	—
D. aquatica	MFLUCC 15-0374^{T}	NR_154040	KU376268	—
	SNJ14	**MH555360**	—	—
D. fluminicola	MFLUCC 15-0417^{T}	NR_154041	KU376270	—
D. guttulata	MFLUCC 16-0183	MF077543	MF077554	MF077532

D. "*leonensis*"	HKUCC 10822	—-	DQ408566	—-
D. longispora	**HFJAU 0705[T]**	**MH555359**	**MH555431**	**MH555357**
D. martinii	HSAUP myr4280	KU999975	KX033566	KX033537
D. multiseptata	MFLUCC 15-0609[T]	NR_154017	KX710140	MF077540
	MFLUCC 16-1044	MF077544	MF077555	MF077533
D. phangngaensis	MFLUCC 16-0857	MF077545	MF077556	MF077534
D. suoluoensis	MFLUCC 17-1305	MF077547	MF077558	MF077536
	MFLUCC 17-0224	MF077546	MF077557	MF077535
D. tectonae	MFLUCC 12-0291	KX751711	KX751713	—
	GZ25	**MH555361**	**—**	**MH555358**
D. tectonigena	MFLUCC 12-0292[T]	NR_154018	KX751714	—
Distoseptispora sp.	HLXM 15-1	—-	KU376269	—-
Dothidea sambuci	AFTOL-ID 274	DQ491505	AY544681	AY544722
Ellisembia bambusicola	HKUCC 3578	—	DQ408562	—
E. calyptrata	HKUCC 10821	—	DQ408564	—
E. minigelatinosa	NN47497	—	DQ408567	—
Ellisembia sp.	HKUCC 10558	—	DQ408565	—
Sporidesmium aquaticivaginatum	MFLUCC 15-0624	KX710147	KX710142	MF077541
S. aquaticum	MFLUCC 15-0420	—	KU376273	—
S. australiense	HKUCC 10833	—	DQ408554	—
S. fluminicola	MFLUCC 15-0346	—	KU376271	—
S. macrurum	HKUCC 2740	—	DQ408555	—
S. obclavatulum	HKUCC 10834	—	DQ408556	—
S. olivaceoconidium	MFLUCC 15-0380	KX710144	KX710139	MF077542
S. pachyanthicola	HKUCC 10835	—	DQ408557	—
S. parvum	HKUCC 10836	—	DQ408558	—
S. pyriformatum	MFLUCC 15-0620[T]	KX710146	KX710141	—
	MFLUCC 15-0627	KX710148	—	KX710143
S. submersum	MFLUCC 15-0421	—	KU376272	—
S. tengii	HKUCC 10837	—	DQ408559	—
S. thailandense	MFLUCC 15-0964[T]	MF374361	MF374370	—
S. tropicale	MFLUCC 16-0185	MF077551	MF077562	MF077539
	HKUCC 10838	—	DQ408560	—
Sporidesmium sp.	KUFA 0043	KT824799	—-	—
Sporidesmium sp.	MFLUCC 15-0617	MF077550	MF077561	—-
Sporidesmium sp.	MFLUCC 16-0186	MF077549	MF077560	MF077538

transcribed spacer (ITS) with the primer pair ITS1 & ITS4 (White & al. 1990), partial small subunit (SSU) with NS1 & NS4 (White & al. 1990), and large subunit (LSU) with LR0R & LR6 (Vilgalys & Hester 1990, Rehner & Samuels 1995). PCR protocols followed the conditions set by Hu & al. (2012b). The PCR products were purified and sequenced by the same primers used for PCR at Sangon Biotech (Shanghai) Co. Ltd.

In this study, we generated six novel sequences (MH555360, MH555359, MH555431, MH555357, MH555361 & MH555358) and retrieved 36 reference sequences from GenBank (Table 1) that were aligned using MAFFT v7.

The ML analyses were produced with RAxML v7.2.6 (Stamatakis & Alachiotis 2010) using a GTRGAMMA substitution model with 1000 bootstrap replicates and evaluated by bootstrap support (MLBS).

The best-fit evolutionary models were estimated using MrModeltest V2.2. Posterior probabilities (PP) (Zhaxybayeva & Gogarten 2002) were determined by Markov chain Monte Carlo sampling (BMCMC) in MrBayes 3.0b4 (Huelsenbeck & Ronquist 2001). Six simultaneous Markov chains were run 1,500,000 generations, with trees sampled every 100 generations and the first 25% deleted as burn-in. Posterior probabilities were calculated based on the remaining trees. The novel taxonomic descriptions and nomenclature were deposited in MycoBank (http://www.mycobank.org/).

Phylogenetic results

The six new sequences generated in our study included one LSU, two SSU, and three ITS sequences. The phylogenetic tree based on the three-locus analysis (Fig. 1) shows the relationship between the new taxon and other related species. The concatenated aligned dataset comprised 17 isolates from 13 *Distoseptispora* spp., 23 isolates from 21 *Sporidesmium* (or "*Ellisembia*") spp., and one isolate of *Dothidea sambuci* (Pers.) Fr. (*Dothideomycetes*) as an outgroup. The dataset including alignment gaps comprised 2817 characters: 1348 for SSU, 629 for ITS, and 840 for LSU. The combined dataset ML tree (Fig. 1) with bootstrap support values (MLBS) and Bayesian posterior probabilities (BPP) indicates several well-supported clades, with the *Distoseptispora longispora* strain forming a well-supported clade (MLBS = 94%, BPP = 0.68) with other *Distoseptispora* species.

Taxonomy

Distoseptispora longispora H.Y. Song & D.M. Hu **sp. nov.** Fig. 2

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Differs from *Distoseptispora aquatica* by its larger and more septate conidia; and from *D. tectonae* and *D. tectonigena* by its smooth and brown to yellowish brown conidia.

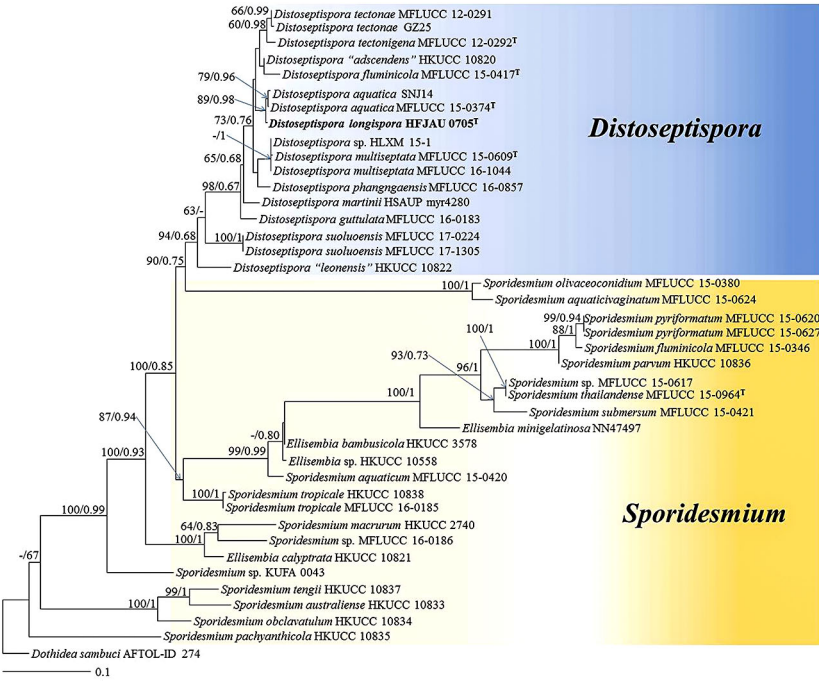
Distoseptispora
Sporidesmium
66/0.99 Distoseptispora tectonae MFLUCC 12-0291
60/0.98 Distoseptispora tectonae GZ25
Distoseptispora tectonigena MFLUCC 12-0292T
Distoseptispora "adscendens" HKUCC 10820
79/0.96 Distoseptispora fluminicola MFLUCC 15-0417T
89/0.98 Distoseptispora aquatica SNJ14
Distoseptispora aquatica MFLUCC 15-0374T
73/0.76 Distoseptispora longispora HFJAU 0705T
-/1 Distoseptispora sp. HLXM 15-1
65/0.68 Distoseptispora multiseptata MFLUCC 15-0609T
Distoseptispora multiseptata MFLUCC 16-1044
98/0.67 Distoseptispora phangngaensis MFLUCC 16-0857
63/- Distoseptispora martinii HSAUP myr4280
Distoseptispora guttulata MFLUCC 16-0183
94/0.68 100/1 Distoseptispora suoluoensis MFLUCC 17-0224
Distoseptispora suoluoensis MFLUCC 17-1305
90/0.75 Distoseptispora "leonensis" HKUCC 10822
100/1 Sporidesmium olivaceoconidium MFLUCC 15-0380
Sporidesmium aquaticivaginatum MFLUCC 15-0624
99/0.94 Sporidesmium pyriformatum MFLUCC 15-0620
100/1 88/1 Sporidesmium pyriformatum MFLUCC 15-0627
100/1 Sporidesmium fluminicola MFLUCC 15-0346
Sporidesmium parvum HKUCC 10836
93/0.73 96/1 Sporidesmium sp. MFLUCC 15-0617
100/1 Sporidesmium thailandense MFLUCC 15-0964T
Sporidesmium submersum MFLUCC 15-0421
100/0.85 87/0.94 Ellisembia minigelatinosa NN47497
-/0.80 Ellisembia bambusicola HKUCC 3578
99/0.99 Ellisembia sp. HKUCC 10558
100/0.93 Sporidesmium aquaticum MFLUCC 15-0420
100/1 Sporidesmium tropicale HKUCC 10838
Sporidesmium tropicale MFLUCC 16-0185
100/0.99 Sporidesmium macrurum HKUCC 2740
64/0.83 100/1 Sporidesmium sp. MFLUCC 16-0186
-/67 Ellisembia calyptrata HKUCC 10821
Sporidesmium sp. KUFA 0043
99/1 Sporidesmium tengii HKUCC 10837
100/1 Sporidesmium australiense HKUCC 10833
Sporidesmium obclavatulum HKUCC 10834
Sporidesmium pachyanthicola HKUCC 10835
Dothidea sambuci AFTOL-ID 274
0.1

Fig. 1. Maximum Likelihood (ML) phylogenetic tree of *Distoseptispora longispora* and allied species based on concatenated SSU–ITS–LSU data. The RAxML bootstrap support values (MLBS) and Bayesian posterior probabilities (BPP) are given at the nodes (MLBS/BPP).

Type: China, Yunnan Province: Mengla, a small stream, on submerged wood, 13 Apr 2017, H.Y. Song (**Holotype**, HFJAU 0705).

Etymology: *longispora*, referring to the long conidia of the fungus.

Colonies on submerged wood superficial, effuse, scattered, hairy, brown to dark brown. Mycelium mostly immersed, composed of branched, septate, smooth, subhyaline to pale brown hyphae. Conidiophores macronematous, mononematous, 2–4-septate, unbranched, single, straight or slightly flexuous, erect, cylindrical, smooth, brown to dark brown, 17–37 × 6–10 µm. Conidiogenous cells monoblastic, integrated, determinate, terminal, light brown to dark brown, cylindrical. Conidial secession schizolytic. Conidia acrogenous, solitary, dry, obclavate, elongated, straight or slightly curved, rounded at the apex, truncate at the base, 31–56-distoseptate, smooth, brown

to yellowish brown, slightly paler towards the apex, 189–297 × 16–23 μm (mean = 204 × 21 μm, n = 50).

Additional specimen examined: **CHINA**, **Yunnan Province**, **Mengla**, a small stream, on submerged wood, 13 Apr 2017, H.Y. Song (HFJAU 0706).

Notes: *Distoseptispora longispora* is characterized by its macronematous, mononematous, septate conidiophores, monoblastic, integrated, determinate, terminal conidiogenous cells, and acrogenous, solitary, dry, obclavate, elongated, distoseptate conidia, which fit well with the generic concepts of *Distoseptispora* (Su & al. 2016). The molecular phylogeny (Fig. 1) clusters the *D. longispora* strain well within the *Distoseptispora* clade and closely related to *D. aquatica* but with an ITS six base pair (bp) difference separating it from *D. aquatica* (MFLUCC 15-0374). *Distoseptispora longispora* resembles *D. aquatica*, *D. tectonae,* and *D. tectonigena* in conidial shape. However, its larger and more septate conidia separate *D. longispora* from *D. aquatica* (189–297 × 16–23 μm; 15–28 septa). In addition, *D. tectonae* has verruculose, dark reddish conidia, and *D. tectonigena* has dark reddish-brown conidia (Hyde & al. 2016).

The multilocus molecular phylogeny and morphological data fully support separation of our new species, *D. longispora*. Morphologically, *Distoseptispora* resembles *Ellisembia* Subram., first established to accommodate the species with distoseptate conidia in *Sporidesmium* Link (Subramanian 1992). However, a molecular phylogeny by Shenoy & al. (2006) showed that *Ellisembia* and *Sporidesmium* were polyphyletic. Su & al. (2016) later clarified differences between *Ellisembia* and *Sporidesmium,* noting that euseptate/distoseptate characters were not supported by molecular evidence and treating *Ellisembia* as a synonym of *Sporidesmium*. *Distoseptispora* species differ from *Ellisembia* (*Sporidesmium*) species in having relatively short conidiophores and darker conidia with slightly paler, but not hyaline, rounded apices, basal cells cut off by cross walls, and of indeterminate length (Su & al. 2016).

There are various hyphomycetes in freshwater habitats, and several studies have reported *Distoseptispora* species, e.g., *D. aquatica*, *D. fluminicola*, *D. guttulata*, *D. multiseptata*, *D. phangngaensis,* and *D. suoluoensis* (Hu & al. 2007, 2010a,b; Huang & al. 2018; Hyde & al. 2016; Su & al. 2016; Yang & al. 2018). Most of these species were identified based on morphology, which proved to be insufficient for accurate identification (Hu & al. 2017). Numerous other studies (Réblová & al. 2016, Su & al. 2016, Zhang & al. 2017) have revealed many different freshwater lineages using molecular analyses.

Fig. 2. *Distoseptispora longispora* (holotype, HFJAU 0705). a. Colonies on submerged wood; b, c. Conidia; d. Conidiophore. Scale bars: a = 100 μm, b–d = 5 μm.

Key to *Distoseptispora* species

1. Conidia muriform, having both longitudinal and transverse septa ..... *D. martinii*
1. Conidia with only transverse septa 2
2. Conidia euseptate 3
2. Conidia distoseptate 4
3. Conidia 75–130 × 7–11 µm, 11–14(–20)-euseptate, smooth ..... *D. guttulata*
3. Conidia 80–125 × 8–13 µm, 8–10-euseptate, verrucose ..... *D. suoluoensis*
4. Conidiogenous cells polyblastic, conidia 35–180 × 7–11 µm ..... *D. palmarum*
4. Conidiogenous cells monoblastic 5
5. Conidiophores having percurrently proliferating conidiogenous cells at the apex of conidiophores 6
5. Conidiophores not as above 7
6. Conidia 115–155 × 9–11 µm ..... *D. rostrata*
6. Conidia 148–225 × 11–12 µm ..... *D. tectonigena*
7. Conidia verruculose, 7.5–9.5 × 3.5–5 µm ..... *D. tectonae*
7. Conidia not verruculose 8
8. Conidia 3–5-distoseptate, 17–30 × 7.5–10 µm ..... *D. dehongensis*
8. Conidia with more than 6 distosepta 9
9. Saprobic on submerged wood in freshwater habitats 12
9. Not saprobic on submerged wood in freshwater habitats 10
10. Saprobic on dead culms of *Thysanolaena maxima*, conidia 8–14-distoseptate, 21.5–80 × 6.5–12.8 µm ..... *D. thysanolaenae*
10. Saprobic on dead leaves of *Pandanus* sp. 11
11. Conidia reddish brown to brown, 130–230 × 13.5–17 µm ..... *D. thailandica*
11. Conidia green-brown to brown, 160–305 × 8–15 µm ..... *D. xishuangbannaensis*
12. Conidia 9–11-distoseptate, 53–71 × 12–16 µm ..... *D. obpyriformis*
12. Conidia with more than 12 distosepta 13
13. Conidiogenous cells yellow, conidia 125–250 × 13–15 µm ..... *D. fluminicola*
13. Conidiogenous cells brownish 14
14. Conidia brown to yellowish brown, 31–56-distoseptate, 189–297 × 16–23 µm ..... *D. longispora*
14. Conidia greenish brown or dark olivaceous green 15
15. Conidiogenous cells subhyaline to pale brown, conidia 58–166 × 10–14 µm ..... *D. cangshanensis*
15. Conidiogenous cells brown to dark brown 16
16. Conidiogenous cells dark brown to olivaceous, conidia 110–157 × 13.5–16.5 µm ..... *D. aquatica*
16. Conidiogenous cells brown 17

17. Conidia dark olivaceous green, multi-distoseptate, 95–290 × 11–20 µm ..... *D. multiseptata*
17. Conidia dark or mid olivaceous to mid or dark brown 18
18. Conidia dark olivaceous to mid or dark brown, 165–350 × 14–19 µm ..... *D. phangngaensis*
18. Conidia mid-olivaceous to brown, 95–123 ×15–19 µm ..... *D. submersa*

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Literature cited

Huang J-E, Song H-Y, Huang X-G, Ma J, Hu D-M. 2018. *Phaeomonilia aquatica* sp. nov., an aquatic hyphomycete from China. Mycotaxon 132: 919–923. https://doi.org/10.5248/132.919

Huelsenbeck JP, Ronquist FR. 2001. MrBayes: Bayesian inference of phylogenetic trees. Biometrics 17: 754–755. https://doi.org/10.109

Hu DM, Zhu H, Cai L, Hyde KD, Zhang KQ. 2007. *Sirothecium triseriale*, a new chirosporous anamorphic species from China. Cryptogamie, Mycologie 28: 311–314.

Hu DM, Cai L Chen H, Bahkali AH, Hyde KD. 2010a. Four new freshwater fungi associated with submerged wood from Southwest Asia. Sydowia 62: 191–203.

Hu DM, Cai L Chen H, Bahkali AH, Hyde KD. 2010b. Fungal diversity on submerged wood in a tropical stream and an artificial lake. Biodiversity and Conservation 19: 3799–3808. https://doi.org/10.1007/s10531-010-9927-5

Hu DM, Cai L, Bahkali AH, Hyde KD. 2012a. Two new freshwater species of *Annulatascaceae* from China. Mycotaxon 120: 81–88. https://doi.org/10.5248/120.81

Hu DM, Cai L, Hyde KD. 2012b. Three new ascomycetes from freshwater in China. Mycologia 104: 1478–1489. https://doi.org/10.3852/11-430

Hu DM, Chen H, Cai L, Bahkali AH, Hyde KD. 2012c. *Aquapeziza*: a new genus from freshwater, and its morphological and phylogenetic relationships to *Pezizaceae*. Mycologia 104: 540–546. https://doi.org/10.3852/11-123

Hu DM, Wang M, Cai L. 2017. Phylogenetic assessment and taxonomic revision of *Mariannaea*. Mycological Progress 16: 271–283. https://doi.org/10.1007/s11557-016-1252-2

Huang J-E, Song H-Y, Ma J, Guan G-X, Hu D-M. 2016. *Xylohyphopsis aquatica* sp. nov., a new aquatic hyphomycete from China. Mycotaxon 131: 391–394. https://doi.org/10.5248/131.3913/bioinformatics/17.8.754

Hyde KD, Hongsanan S, Jeewon R & al. 2016. Fungal diversity notes 367-490: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 80: 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde KD, Tennakoon DS, Jeewon R & al. 2019. Fungal diversity notes 1036–1150: taxonomic and phylogenetic contributions on genera and species of fungal taxa. Fungal Diversity, 96: 1–242. https://doi.org/10.1007/s13225-019-00429-2

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Molecular Biology and Evolution 30: 772–780. https://doi.org/10.1093/molbev/mst010

Luo Z-L, Hyde KD, Bhat DJ, Jeewon R, Maharachchikumbura SSN, Bao D-F & al. 2018. Morphological and molecular taxonomy of novel species *Pleurotheciaceae* from freshwater habitats in Yunnan, China. Mycological Progress 17(5): 511–530. https://doi.org/10.1007/s11557-018-1377-6

Phookamsak R, Hyde KD, Jeewon R & al. 2019. Fungal diversity notes 929–1035: taxonomic and phylogenetic contributions on genera and species of fungi. Fungal Diversity 95: 1–273. https://doi.org/10.1007/s13225-019-00421-w

Réblová M, Fournier J, Štěpánek V. 2016. Two new lineages of aquatic ascomycetes: *Atractospora* gen. nov. and *Rubellisphaeria* gen. et sp. nov., and a sexual morph of *Myrmecridium montsegurinum* sp. nov. Mycological Progress 15: 21. https://doi.org/10.1007/s11557-016-1166-z

Rehner SA, Samuels GJ. 1995. Molecular systematics of the *Hypocreales*: a teleomorph gene phylogeny and the status of their anamorphs. Canadian Journal of Botany 73: 816–823. https://doi.org/10.1139/b95-327

Shenoy BD, Jeewon R, Wu WP, Bhat DJ, Hyde KD. 2006. Ribosomal and RPB2 DNA sequence analyses suggest that *Sporidesmium* and morphologically similar genera are polyphyletic. Mycological Research 110: 916–928. https://doi.org/10.1016/j.mycres.2006.06.004

Song HY, Zhong PA, Liao JL, Wang ZH, Hu DM, Huang YJ. 2018. *Junewangia aquatica* (*Junewangiaceae*), a new species from freshwater habitats in China. Phytotaxa 336: 272–278. https://doi.org/10.11646/phytotaxa.336.3.5

Stamatakis A, Alachiotis N. 2010. Time and memory efficient likelihood-based tree searches on phylogenomic alignments with missing data. Bioinformatics 26: i132–i139. https://doi.org/10.1093/bioinformatics/btq205

Su H, Hyde KD, Maharachchikumbura SSN, Ariyawansa HA, Luo Z & al. 2016. The families *Distoseptisporaceae* fam. nov., *Kirschsteiniotheliaceae*, *Sporormiaceae* and *Torulaceae*, with new species from freshwater in Yunnan Province, China. Fungal Diversity 80: 375–409. https://doi.org/10.1007/s13225-016-0362-0

Subramanian C. 1992. A reassessment of *Sporidesmium* (*Hyphomycetes*) and some related taxa. Proceedings of the National Academy of Sciences, India, Section B: Biological Sciences 58: 179–190.

Tibpromma S, Hyde KD, McKenzie EHC & al. 2018. Fungal diversity notes 840–928: micro-fungi associated with *Pandanaceae*. Fungal Diversity 93: 1–160. https://doi.org/10.1007/s13225-018-0408-6

Vilgalys R, Hester M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

White TJ, Bruns T, Lee S, Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA Innis & al. (eds). PCR Protocols: a Guide to Methods and Applications. San Diego, Academic Press. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Xia JW, Ma YR, Li Z, Zhang XG. 2017. *Acrodictys*-like wood decay fungi from southern China, with two new families *Acrodictyaceae* and *Junewangiaceae*. Scientific Reports 7: 7888. https://doi.org/10.1038/s41598-017-08318-x

Yang J, Maharachchikumbura SSN, Liu J-K, Hyde KD, Jones EBG, Al-Sadi AM, Liu Z-Y. 2018. *Pseudostanjehughesia aquitropica* gen. et sp. nov. and *Sporidesmium sensu lato* species from freshwater habitats. Mycological Progress 17: 591–616. https://doi.org/10.1007/s11557-017-1339-4

Zhang H, Dong W, Hyde KD, Maharachchikumbura SS, Hongsanan S, Bhat DJ, Al-Sadi AM, Zhang D. 2017. Towards a natural classification of *Annulatascaceae*-like taxa: introducing *Atractosporales* ord. nov. and six new families. Fungal Diversity 85: 75–110. https://doi.org/10.1007/s13225-017-0387-z

Zhaxybayeva O, Gogarten JP. 2002. Bootstrap, Bayesian probability and maximum likelihood mapping: exploring new tools for comparative genome analyses. BMC Genomics 3: 4. https://doi.org/10.1186/1471-2164-3-4